

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 1, 2005, 13:07:33 ; Search time 161.5 Seconds
(without alignments)
4125.597 Million cell updates/sec

Title: US-10-659-782A-11
Perfect score: 1030
Sequence: 1 actctggatgggtgctgttt.....tggcagcagggaggggtgggg 579

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q/cgn2.1/USPTO spool_p/US10659782/runat_01022005_130352_14253/app_query.fasta_1.775
-DB=UniProt_02 -OFMT=fastan -SUFFIX=runat -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10659782 @CIGN_1_1_244 @runat_01022005_130352_14253 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|------------|---------------------|
| 1 | 326 | 31.7 | 91 | Q86YP8 | Q86YP8 homo sapien |
| 2 | 326 | 31.7 | 117 | GHRL HUMAN | Q9ub03 homo sapien |
| 3 | 308 | 29.9 | 117 | Q6UDE7 | Q6ude7 macaca mula |
| 4 | 308 | 29.9 | 117 | AAQ74381 | AAQ74381 macaca mu |
| 5 | 308 | 29.9 | 117 | AAQ74837 | AAQ74837 macaca mu |
| 6 | 265 | 25.7 | 117 | Q8CH53 | Q8ch53 meriones un |
| 7 | 257 | 25.0 | 86 | Q811T4 | Q811t4 mus musculus |
| 8 | 257 | 25.0 | 117 | GHRL MOUSE | Q9eqx0 mus musculus |
| 9 | 256 | 24.9 | 117 | GHRL RAT | Q9qy77 rattus norv |
| 10 | 237 | 23.0 | 117 | GHRL CANFA | Q9bef8 canis fam |
| 11 | 237 | 23.0 | 117 | BAC75929 | Bac75929 canis fam |
| 12 | 232.5 | 22.6 | 118 | GHRL PIG | Q9gky5 sus scrofa |
| 13 | 209.5 | 20.3 | 116 | GHRL BOVIN | Q9bdj6 bos taurus |
| 14 | 206.5 | 20.0 | 116 | Q863L0 | Q863l0 ovine aries |
| 15 | 182.5 | 17.7 | 65 | Q6TGF0 | Q6tgf0 sus scrofa |
| 16 | 182.5 | 17.7 | 65 | AAQ97622 | AAQ97622 sus scrofa |

| | | | | | | |
|----|-------|------|------|---|------------|---------------------------|
| 17 | 162.5 | 15.8 | 97 | 2 | Q863C6 | Q863c6 ovine aries |
| 18 | 158.5 | 15.4 | 78 | 2 | Q7SD1 | Q7edl1 mus musculus |
| 19 | 147 | 14.3 | 54 | 2 | Q6SLG1 | Q6slg1 capra hircus |
| 20 | 147 | 14.3 | 54 | 2 | AA67351 | AA67351 capra hircus |
| 21 | 146 | 14.2 | 54 | 2 | Q6SLF6 | Q6slf6 cervus elaphus |
| 22 | 146 | 14.2 | 54 | 2 | AA67355 | AA67355 cervus elaphus |
| 23 | 145 | 14.1 | 52 | 2 | Q6SLF9 | Q6slf9 odocoileus |
| 24 | 145 | 14.1 | 52 | 2 | AA67361 | AA67361 odocoileus |
| 25 | 145 | 14.1 | 54 | 2 | Q6SLF2 | Q6slf2 odocoileus |
| 26 | 145 | 14.1 | 54 | 2 | Q6SLF8 | Q6slf8 rangifer tarandus |
| 27 | 145 | 14.1 | 54 | 2 | AA67353 | AA67353 rangifer tarandus |
| 28 | 145 | 14.1 | 54 | 2 | AA67359 | AA67359 odocoileus |
| 29 | 142 | 13.8 | 54 | 2 | Q6SLF4 | Q6slf4 alces alces |
| 30 | 142 | 13.8 | 54 | 2 | AA67357 | AA67357 alces alces |
| 31 | 133 | 12.9 | 54 | 2 | Q6SLG3 | Q6slg3 ovine aries |
| 32 | 133 | 12.9 | 54 | 2 | AA67349 | AA67349 ovine aries |
| 33 | 130 | 12.6 | 54 | 2 | Q6SPC2 | Q6spc2 bison bison |
| 34 | 130 | 12.6 | 54 | 2 | AA10495 | AA10495 bison bison |
| 35 | 126.5 | 12.3 | 54 | 2 | Q6SLG5 | Q6slg5 kogia brevicauda |
| 36 | 126.5 | 12.3 | 54 | 2 | Q6SLG7 | Q6slg7 bos taurus |
| 37 | 126.5 | 12.3 | 54 | 2 | AA67345 | AA67345 bos taurus |
| 38 | 126.5 | 12.3 | 54 | 2 | AA67347 | AA67347 kogia brevicauda |
| 39 | 112 | 10.9 | 213 | 2 | Q6YWA5 | Q6ywa5 oryza sativa |
| 40 | 112 | 10.9 | 213 | 2 | BAD17581 | BAD17581 oryza sativa |
| 41 | 112 | 10.5 | 262 | 2 | Q6ZMW4 | Q6znm4 homo sapien |
| 42 | 112 | 10.5 | 262 | 2 | BAC85372 | BAC85372 homo sapien |
| 43 | 112 | 10.9 | 1255 | 1 | MUC1 HUMAN | P15941 h mucin 1 p |
| 44 | 110.5 | 10.7 | 550 | 2 | Q6SPE9 | Q6spe9 oryctolagus |
| 45 | 110.5 | 10.7 | 550 | 2 | AA24088 | AA24088 oryctolagus |

ALIGNMENTS

RESULT 1

Q86YP8 PRELIMINARY; PRT; 91 AA.
AC Q86YP8;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DE Exon 3-deleted preproghrelin variant.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeffery P.L., Herington A.C., Chopin L.K.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY184207; AAO27351.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016608; P:growth hormone-releasing hormone activity; IEA.
DR GO; GO:0050791; P:regulation of physiological process; IEA.
DR InterPro; IPR006738; motifin ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04644; Motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
SQ SEQUENCE 91 AA; 9972 MW; E7E532D32A3F8609 CRC64;

Alignment Scores:
Pred. No.: 1,928-18 Length: 91
Score: 326.00 Matches: 74
Percent Similarity: 53.19% Conservative: 1
Best Local Similarity: 52.48% Mismatches: 1
Query Match: 31.65% Indels: 66
DB: 2 Gaps: 1

US-10-659-782A-11 (1-579) x Q86YP8 (1-91)

QY 112 ATGCGCTCCCGAGGACCGCTCTGCAGCTCTGCTCGGCATGCTCTGGCTGACTTG 171
|||||
DB 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20

QY 172 GCCATGCGAGCTCCAGCTTCTGAGCCCTGACACACAGAGTCCAGGTGAGACCTCC 231
 Db |||||
 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
 QY 232 CACAAGACCCCATGTTCTTCAGCCCTGCGCACTTAGCAACACAGCTCTGTGACCTGGAG 291
 Db ----- 37
 QY 292 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGACAAAGGACTCTGGGTCTTGAC 351
 Db ----- 37
 QY 352 CTCACGTGTTCTGGAAGACATGCGGCTTAGAGTCTTAACAGACTGTTTCCCCCTTCC 411
 Db ----- 37
 QY 412 AGCAGAGAAGGTCGAGAGCTCAAGCAGACCAAGCTCAGCCGCGAGCTCTAGCAGCTTACAGGCT 471
 Db |||||-----ArgLysGluSerLysLysProProAlaLysLeuGlnProArgAlaLeuAlaGlyT 56
 QY 472 GGCCTCGCCGGAAGATGAGGTCAAGCAGAGGCGCAGAGGATCACTGGAAGTCCGG 530
 Db |||||----- 56
 56 rpleuArgProGluAspGlyGlyGlnAlaGluGlyAlaGluAspGluLeuGluValArg 75
 RESULT 2
 GHRL_HUMAN STANDARD; PRT; 117 AA.
 ID AC Q9UBU3; Q8TAT9; Q9H3R3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
 DE releasing peptide) (Motilin-related peptide) (M46 protein)
 DE (UNQ524/PRO1066).
 GN Name=GHRL; Synonyms=MTLPR;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND ACYLATION OF SER-26.
 RX MEDLINE=20067959; PubMed=10604470; DOI=10.1038/45230;
 RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
 RT "Ghrelin is a growth-hormone-releasing acylated peptide from
 RT stomach.";
 RL Nature 402:656-660(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RA Kojima M.;
 RL Submitted (DEC-1999) to the ENBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Stomach;
 RA Tomasetto C., Karam S.M., Rio M.-C.;
 RT "Identification of a novel gastric protein m46.";
 RL Submitted (JAN-2000) to the ENBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Wajnarajch M.P., Ten I.S., Gertner J.M., Leibell R.L.;
 RT "Genomic organization of the human Ghrelin gene.";
 RL J. Endocr. Genet. 1:231-233(2000).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.;

"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
 Genome Res. 13:2265-2270(2003).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 24-33.
 RC TISSUE=Stomach;
 RX MEDLINE=20389976; PubMed=10930375;
 RA Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O.,
 RA Staub A., Alexander G., Chenard M.-P., Rio M.-C.;
 RT "Identification and characterization of a novel gastric peptide
 RT hormone: the motilin-related peptide.";
 RL Gastroenterology 119:395-405(2000).
 RN [8]
 RP SEQUENCE OF 24-38.
 RA Zhang Z., Henzel W.;
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites.";
 RL Submitted (JUN-2004) to Swiss-Prot.
 RN [9]
 RP REVIEW.
 RX MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
 RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 RT "Ghrelin: discovery of the natural endogenous ligand for the growth
 RL hormone secretagogue receptor.";
 Trends Endocrinol. Metab. 12:118-122(2001).
 CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
 CC receptor type 1 (GHSR) inducing the release of growth hormone from
 CC the pituitary. Has an appetite-stimulating effect, induces
 CC adiposity and stimulates gastric acid secretion. Involved in
 CC growth regulation.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Ghrelin;
 CC IsoId=Q9UBU3-1; Sequence=Displayed;
 CC Name=2; Synonyms=del-Gln14-ghrelin;
 CC IsoId=Q9UBU3-2; Sequence=VSP_003245;
 CC -!- PTM: O-n-octanoylation is essential for activity.
 CC -!- SIMILARITY: Belongs to the motilin family.
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/GhrelinID327.html".

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or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AB029434; BAA89371.1; -
DR EMBL; AB035700; BAB19045.1; -
DR EMBL; AJ252278; CAB65733.1; -
DR EMBL; AF296558; AAG10300.1; -
DR EMBL; AY359053; AAO89412.1; -
DR EMBL; BC025791; AAH25791.1; -
DR PIR; A59316; A59316.
DR MIM; 605353; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005625; C:soluble fraction; TAS.
DR GO; GO:0005131; F:growth hormone receptor binding; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; Motilin_assoc; 1.
DR Pfam; PF04644; Motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD32162; Preproghrelin; 1.
KW Alternative splicing; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Lipoprotein; Signal.
FT SIGNAL 1 23
FT PEPTIDE 24 51 Ghrelin.
FT PROPEP 52 117 Removed in mature form.
FT LIPID 26 26 O-octanoyl serine.
FT VARSPIC 37 37 Missing (in isoform 2).
FT CONFLICT 72 72 /FTID=VSP_003245.
FT SEQUENCE 117 AA; 12911 MW; 39C0572EBECA2755 CRC64;

Alignment Scores:
Pred. No.: 1.96e-18 Length: 117
Score: 326.00 Matches: 74
Percent Similarity: 53.19% Conservative: 1
Best Local Similarity: 52.48% Mismatches: 0
Query Match: 31.65% Indels: 66
DB: 1 Gaps: 1

US-10-659-782a-11 (1-579) x GHRL_HUMAN (1-117)
QY 112 ATGCCCTCCCGAGGACCGTCTGCGAGCTCTGCTCGGATGCTCTGGTGGACTTG 171
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
QY 172 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGAGTCCAGGTGAGACCTCCC 231
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGln--Gln----- 37
QY 232 CACAAAGCCCAATGTTTTCACGCCCTGCCACTTAGCAACCACTCTGTGACCTGGAG 291
Db 37 ----- 37
QY 292 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 351
Db 37 ----- 37
QY 352 CTCACCTGTTTCTGGAAGGACATGGGGCTTAGAGTCTTAACACAGACTGTTTCCCTTCC 411
Db 37 ----- 37
QY 412 AGCAGAGAAAGAGTCTGAAGAGCCACAGCAAGCTCAGCCCCGAGCTCTAGCAGGCT 471
Db 38 -----ArgLysGluSerLysProProAlaLysLeuGlnProArgAlaLeuAlaGlyT 56
QY 472 GCCTCCGCCCGAAGATGAGTCAAGCAAGAGGGCGAGAGATGAACCTGGAAGTCCGG 530
Db 56 rpLeuArgProGluAspGlyGlyGlnAlaGluGlyAlaGluAspGluLeuValArg 75

RESULT 3
Q6UDE7

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ID Q6UDE7 PRELIMINARY; PRT; 117 AA.
AC Q6UDE7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ghrelin.
GN Name=GHRL;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]_
RP SEQUENCE FROM N.A.
RX PubMed14736731;
RA Angeloni S.V., Glynn N., Ambrosini G., Garant M.J., Dee Higley J.,
RA Suomi S., Hansen B.C.;
RT "Characterization of the rhesus monkey ghrelin gene and factors
RT influencing ghrelin gene expression and fasting plasma levels.";
RL Endocrinology 145:2197-2205(2004).
DR EMBL; AY372274; AAQ74837.1; -.
DR EMBL; AY371699; AAQ74381.1; -.
DR InterPro; IPR006737; motilin_assoc.
DR InterPro; IPR006738; motilin_ghrelin.
DR InterPro; IPR005441; Preproghrelin.
DR Pfam; PF04643; Motilin_assoc; 1.
DR Pfam; PF04644; Motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
DR ProDom; PD32162; Preproghrelin; 1.
SQ SEQUENCE 117 AA; 12913 MW; 1B634ACE1E1F19FF CRC64;

Alignment Scores:
Pred. No.: 6.06e-17 Length: 117
Score: 308.00 Matches: 70
Percent Similarity: 51.06% Conservative: 2
Best Local Similarity: 49.65% Mismatches: 3
Query Match: 29.90% Indels: 66
DB: 2 Gaps: 1

US-10-659-782a-11 (1-579) x Q6UDE7 (1-117)
QY 112 ATGCCCTCCCGAGGACCGTCTGCGAGCTCTGCGAGCTCTGCTCGGATGCTCTGGTGGACTTG 171
Db 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
QY 172 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGAGTCCAGGTGAGACCTCCC 231
Db 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArg--Ala----- 35
QY 232 CACAAAGCCCAATGTTTTCACGCCCTGCCACTTAGCAACCACTCTGTGACCTGGAG 291
Db 35 ----- 35
QY 292 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 351
Db 35 ----- 35
QY 352 CTCACCTGTTTCTGGAAGGACATGGGGCTTAGAGTCTTAACACAGACTGTTTCCCTTCC 411
Db 36 -----G 36
QY 412 AGCAGAGAAAGAGTCTGAAGAGCCACAGCAAGCTCAGCCCCGAGCTCTAGCAGGCT 471
Db 36 lnGlnArgLysGluSerLysProProAlaLysLeuGlnProArgAlaLeuAlaGlyT 56
QY 472 GCCTCCGCCCGAAGATGAGTCAAGCAAGAGGGCGAGAGATGAACCTGGAAGTCCGG 530
Db 56 rpLeuArgProGluAspGlyGlyGlnAlaGluGlyAlaGluAspGluLeuGluLeuGln 75

RESULT 4
AAQ74381
ID AAQ74381 PRELIMINARY; PRT; 117 AA.
AC AAQ74381;

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| | | | | | |
|----------------------------------------------|----------|---------------|-----|--|--|
| Alignment Scores: | | | | | |
| Pred. No.: | 6.06e-17 | Length: | 117 | | |
| Score: | 308.00 | Matches: | 70 | | |
| Percent Similarity: | 51.06% | Conservative: | 2 | | |
| Best Local Similarity: | 49.65% | Mismatches: | 3 | | |
| Query Match: | 29.90% | Indels: | 66 | | |
| DB: | 2 | Gaps: | 1 | | |
| US-10-659-782A-11 (1-579) x AAQ74837 (1-117) | | | | | |

| | | | |
|----|-----|------------------------------------------------------------------|-----|
| Qy | 112 | ATGCCCTCCGAGGACGGTCTGAGCCCTCTGCTCTCCGCAATGCTCTGGCTGACCTTG | 171 |
| Db | 1 | MecProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu | 20 |
| Qy | 172 | GCCATGCGACGGCTCCAGCTTCTGAGCCCTGAAACACGAGAGAGTCCAGGTGAGACCTCC | 231 |
| Db | 21 | AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArg--Ala----- | 35 |
| Qy | 232 | CACAAAGCCCCACATGTTGTTTCCAGCCCTGCCACTTACCAACCAACAGCTCTGTGACCTGGAG | 291 |

| | | | |
|----|-----|----------------------------------------------------------|-----|
| Db | 35 | ----- | 35 |
| Qy | 292 | CAGCAGCGCATCTCTGGGCTTCAGTCTTCTCCAGACACAAAGGACTCTGGTGTGAC | 351 |
| Db | 35 | ----- | 35 |
| Qy | 352 | CTCACTGTTCTTGGAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTCC | 411 |
| Db | 36 | ----- | 16 |

| | | |
|--------|-------------------------------------------|-----------------------------------------|
| Q8CH53 | PRELIMINARY; | PRT; 117 AA. |
| ID | Q8CH53 | |
| AC | Q8CH53; | |
| DT | 01-MAR-2003 | (T-EMBLrel. 23, Created) |
| DT | 01-MAR-2003 | (T-EMBLrel. 23, Last sequence update) |
| DT | 01-JUN-2003 | (T-EMBLrel. 24, Last annotation update) |
| DE | Chrelin preproprotein. | |
| OS | Meriones uroguiculatus (Mongolian gerbil) | |

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RN SEQUENCE FROM N.A.
RP Suzuki H., Ota T., Masaoka T., Miyazawa M., Amagai M., Nishikawa T.,
RA Ishii H.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF442491; AAC06965.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA.
DR GO; GO:0050791; P:regulation of physiological process; IEA.
DR InterPro; IPR006737; motifin assoc.
DR InterPro; IPR006738; motifin_ghrelin.
DR

Alignment Scores:
Pred. No.: 9.8e-13 Length: 86
Score: 257.00 Matches: 60
Percent Similarity: 46.81% Conservative: 6
Best Local Similarity: 42.55% Mismatches: 9
Query Match: 24.95% Indels: 66
DB: 2 Gaps: 1

US-10-659-782A-11 (1-579) x Q811T4 (1-86)

| | | | |
|----|-----|--------------------------------------------------------------|-----|
| Qy | 112 | ATGCCCTCCCGAGGACCGCTGCAGCCTCTCTGCTCCTCGGCATGCTCTGGCTGGACCTTG | 171 |
| Db | 1 | MetLeuSerSerGlyThrIleCysSerLeuLeuLeuLeuSerMetLeuTrpMetAspMet | 20 |
| Qy | 172 | GCCATGGCAGGCTCCAGCTTCTCAGCCCTCAACACACAGAGAGTCCAGGTGAGACCTCC | 231 |
| Db | 21 | AlaMetAlaGlySerSerPheLeuSerProGluHisGlnLys--Ala | 35 |
| Qy | 232 | CACAAAGCCCAACATGTTGTTCCAGCCCTGCCACTTAGCAACAGACTCTGTGACCTGGAG | 291 |
| Db | 35 | ----- | 35 |
| Qy | 292 | CAGCAGGCCCATCTCTGGGCTTCAGTCTTCTCCCAGAGCACAAGGACTCTGGGTCTGAC | 351 |
| Db | 35 | ----- | 35 |
| Qy | 352 | CTCACTGTTTCTGGAAGACATGGGGCTTAGAGTCTAAACAGACTGTTTCCCCCTTCC | 411 |
| Db | 36 | ----- | 36 |
| Qy | 412 | AGCAGAGAAAGAGTTCGAAGAAGCCACGACCAAGCTGCAGCCCGAGCTCTAGCAGGT | 471 |
| Db | 36 | InGlnArgLysGluSerLysLysProProAlaLysLeuGlnProArgAlaLeuGluGlyt | 56 |
| Qy | 472 | GGCTCCGCCCGAAGATGGAGCTCAAGCAGAGAGGGGCAGAGCATGAATGGAGTCCGG | 530 |
| Db | 56 | rpLeuHisProGluAspArgGlyGlnAlaGluGluThrGluGluLeuGluIleArg | 75 |

RESULT 8

ID_GHRL_MOUSE STANDARD; PRT; 117 AA.

| | |
|----|-----------------------------------------------------------------------------------------------------------------------------|
| AC | Q9EQX0; Q9WU21; |
| AD | 28-FEB-2003 (Rel. 41, Created) |
| DT | 28-FEB-2003 (Rel. 41, Last sequence update) |
| DT | 05-JUL-2004 (Rel. 44, Last annotation update) |
| DE | Ghrelin precursor (Growth hormone secretagogue) (Growth hormone releasing peptide) (Motilin-related peptide) (M46 protein). |
| GN | Name=Ghrl; Synonyms=MtLrp; |
| OS | MS musculus (Mouse). |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| OX | NCBI_TaxID=10090; |
| RP | [1] |
| RP | SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SEQUENCE OF 24-30. |
| RP | TISSUE=Stomach; |
| RX | MEDLINE=20389976; PubMed=10930375; |
| RA | Tomasetto C., Karam S.M., Ribieras S., Masson R., Lefebvre O., |
| RA | Staub A., Alexander G., Chenard M.-P., Rio M.-C.; |
| RT | Identification and characterization of a novel gastric peptide hormone: the motilin-related peptide."; |
| RT | Gastroenterology 119:395-405(2000). |
| RL | [2] |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). |
| RP | Kojima M.; |
| RA | "Mouse mRNA for preproghrelin."; |
| RL | Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases. |
| RP | [3] |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). |
| RA | Tanaka M., Hayashida Y., Iguchi T., Nakao N., Nakai N., Nakashima K.; |
| PL | Submitted (APR-2001) to the EMBL/GenBank/DBJ databases. |
| RP | [4] |
| RP | SEQUENCE FROM N.A. (ISOFORM 1). |
| RC | STRAIN=C57BL/6J; TISSUE=Stomach; |

MEDLINE=22354683; PubMed=12465851; DOI=10.1038/nature01266;
 Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
 Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 Varardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 Hara A., Haashizume M., Imotani K., Ishii Y., Itoh M., Kagawa A.,
 Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 Birney E., Hayashizaki Y.,
 Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 Nature 420:563-573(2002).
 [5]
 REVIEW.
 MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
 Kojima M., Hosoda H., Matsuo H., Kangawa K.;
 "Ghrelin: discovery of the natural endogenous ligand for the growth
 hormone secretagogue receptor.";
 Trends Endocrinol. Metab. 12:118-122(2001).
 CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
 receptor type 1 (GHSR) inducing the release of growth hormone from
 the pituitary. Has an appetite-stimulating effect, induces
 adiposity and stimulates gastric acid secretion. Involved in
 growth regulation.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Name=1; Synonyms=Ghrelin;
 IsoId=Q9EQX0-1; Sequence=Displaced;
 Name=2; Synonyms=del-Gln14-ghrelin;
 IsoId=Q9EQX0-2; Sequence=VSP_003246;
 CC -!- TISSUE SPECIFICITY: Mainly expressed in the gastrointestinal tract
 with higher levels in the stomach, medium levels in the duodenum,
 jejunum, ileum and colon. Low expression in the testis and brain.
 CC Not detected in the salivary gland, pancreas, liver and lung.
 CC -!- PTM: O-n-octanoylation is essential for activity (By similarity).
 CC -!- SIMILARITY: Belongs to the motilin family.
 CC
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 CC
 CC EMBL; AJ243503; CAB46500.1; -
 CC EMBL; AB035701; BAB19046.1; -
 CC EMBL; AB060078; BAB9857.1; -
 CC EMBL; AK008658; BAB25814.1; -
 CC EMBL; AK008860; BAB25934.1; -
 CC MGD; MGI:1930008; Ghrl.
 CC GO; GO:0005737; C:cytoplasm; IDA.
 CC GO; GO:0005576; C:extracellular; IDA.
 CC InterPro; IPR006737; motilin_assoc.

RA Kojima M., Hosoda H., Date Y., Nakazato M., Matsuo H., Kangawa K.;
RT "Ghrelin is a growth-hormone-releasing acylated peptide from
RL stomach.";
RN Nature 402:656-660(1999).
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 24-51, MASS
RP SPECTROMETRY, AND ACYLATION OF SER-26.
RC STRAIN-Sprague-Dawley; TISSUE-Stomach;
RX MEDLINE=20357315; PubMed=10801861; DOI=10.1074/jbc.M002784200;
RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
RT "Purification and characterization of rat des-Gln14-ghrelin, a second
RT endogenous ligand for the growth hormone secretagogue receptor.";
RL J. Biol. Chem. 275:21995-22000(2000).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=21092536; PubMed=11162448; DOI=10.1006/bbrc.2000.4039;
RA Hosoda H., Kojima M., Matsuo H., Kangawa K.;
RT "Ghrelin and des-acyl ghrelin: two major forms of rat ghrelin peptide
RT in gastrointestinal tissue.";
RL Biochem. Biophys. Res. Commun. 279:909-913(2000).
RN [4]
RP STRUCTURE-ACTIVITY RELATIONSHIP.
RX MEDLINE=21433488; PubMed=11549267; DOI=10.1006/bbrc.2001.5553;
RA Matsumoto M., Hosoda H., Kitajima Y., Morozumi N., Minamitake Y.,
RA Tanaka S., Matsuo H., Kojima M., Hayashi Y., Kangawa K.;
RT "Structure-activity relationship of ghrelin: pharmacological study of
RT ghrelin peptides.";
RL Biochem. Biophys. Res. Commun. 287:142-146(2001).
RN [5]
RP REVIEW.
RX MEDLINE=21203998; PubMed=11306336; DOI=10.1016/S1043-2760(00)00362-3;
RA Kojima M., Hosoda H., Matsuo H., Kangawa K.;
RT "Ghrelin: discovery of the natural endogenous ligand for the growth
RT hormone secretagogue receptor.";
RL Trends Endocrinol. Metab. 12:118-122(2001).
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue
CC receptor type 1 (GHSR) inducing the release of growth hormone from
CC the pituitary. Has an appetite-stimulating effect, induces
CC adiposity and stimulates gastric acid secretion. Involved in
CC growth regulation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Ghrelin;
CC IsoId=Q9YH7-1; Sequences=Displayed;
CC Name=2; Synonyms=del-Gln14-ghrelin;
CC IsoId=Q9YH7-2; Sequences=VSP 003248;
CC -!- TISSUE SPECIFICITY: Broadly expressed with higher expression in
CC the stomach. Very low levels are detected in the hypothalamus,
CC heart, lung, pancreas, intestine and adipose tissue.
CC -!- PTM: O-n-octanoylation is essential for activity. The replacement
CC of Ser-26 by aromatic tryptophan preserves ghrelin activity.
CC -!- MASS SPECTROMETRY: MW=3314.9; MW ERR=0.7; METHOD=Electrospray;
CC RANGE=24-51 (Q9YH7-1); NOTE=Ref.1
CC -!- MASS SPECTROMETRY: MW=3187.1; MW ERR=0.6; METHOD=Electrospray;
CC RANGE=24-50 (Q9YH7-2); NOTE=Ref.2.
CC -!- SIMILARITY: Belongs to the motilin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AB029433; BAA89370.1; -;
CC DR EMBL; AB035699; BAB11956.1; -;
CC DR PIR; B59316; B59316.
CC DR InterPro; IPR006737; motilin assoc.
CC DR InterPro; IPR006738; motilin ghrelin.
CC DR InterPro; IPR005441; Preproghrelin.
CC Pfam; PF04643; Motilin_assoc; 1.

DR Pfam; PF04644; Motilin_ghrelin; 1.
DR PRINTS; PR01624; GHRELIN
DR PRODOM; PD332162; Preproghrelin; 1.
KW Alternative splicing; Cleavage on pair of basic residues;
KW Direct protein sequencing; Hormone; Lipoprotein; Signal.
FT SIGNAL 1 23 Ghrelin.
FT PEPTIDE 24 51 Removed in mature form.
FT PROPEP 52 117 O-octanoyl serine.
FT LIPID 26 26 Missing (in isoform 2).
FT VARSPIC 37 37 /FTID=VSP 003248.
SQ SEQUENCE 117 AA; 13176 MW; 8857546F851A7691 CRC64;

Alignment Scores:
Pred. No.: 1.22e-12 Length: 117
Score: 256.00 Matches: 60
Percent Similarity: 46.81% Conservative: 6
Best Local Similarity: 42.55% Mismatches: 9
Query Match: 24.85% Indels: 66
DB: 1 Gaps: 1

US-10-659-782A-11 (1-579) x GHRL_RAT (1-117)
QY 112 ATGCCCTCCCGAGGACCGCTCGAGCGCTCTGCTCGGATGCTCTGGTGGACTTG 171
DB 1 MetValSerSerAlaThrIleCysSerLeuLeuLeuSerMetLeuTrpMetAspMet 20
QY 172 GCCATGGCAGCTCCAGTCTCTGAGCCCTGAACACAGAGAGTCCAGGTGAGACTCCC 231
DB 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnLys--Ala----- 35
QY 232 CACAAGCCCGACATGTTGTTCCAGCCCTGCCACTTAGCAACACGCTCTGTGACCTGGAG 291
DB 35 ----- 35
QY 292 CAGCAGCGCCATCTCTGGGCTTCACTTCTCCAGAGCACAAGGACTCTGGGTGTGAC 351
DB 35 ----- 35
QY 352 CTCAGTGTCTTGGAGGACATGCGGGCTTAGAGTCTTAAACAGACTGTTTCCCTTCC 411
DB 36 -----G 36
QY 412 AGCAGAGAAAGAGTCTGAAGAAGCCAGCCAGCTCAGCCCGAGCTCTAGCAGGCT 471
DB 36 InGlnArgLysGluSerLysLysProAlaLysLeuGlnProArgAlaLeuGluGlyT 56
QY 472 GCCTCCGCGCCGAGATGAGTCAAGCAGAGGAGGCGAGAGTCAACTGGAAGTCCGG 530
DB 56 rpLeuHisProGluAspArgGlyGlnAlaGluGluGluGluLeuGluLeuArg 75

RESULT 10
GHRL_CANFA
ID GHRL_CANFA STANDARD; PRT; 117 AA.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ghrelin precursor (Growth hormone secretagogue) (Growth hormone
DE releasing peptide) (Motilin-related peptide).
GN Name=GHRL; Synonyms=MTLRP;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Gastric fundus;
RA Tomasetto C., Wendling C., Rio M.-C., Poitras P.;
RT "Identification of cDNA encoding MTLRP/ghrelin precursor from dog
RT fundus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DDIJ databases.
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue

| | | | |
|----|-----|----------------------------------------------------------------|-----|
| QY | 112 | ATGCCCTCCCGAGGACCGTCTGCAGCCCTCTGCTCTCGGCATGCTCTGGCTG---GAC | 168 |
| DB | 1 | MetProSerThrGlyThrIleCysSerLeuLeuLeuLeuSerValLeuLeuMetAlaAsp | 20 |
| QY | 169 | TTGGCCATGGCAGGCTTCAGCTTCTGTGAGCCCTGAACACCCAGAGAGTCCAGGTGAGACCT | 228 |
| DB | 21 | LeuAlaMetAlaGlySerSerPheLeuSerProGluHisGlnLysValGln---Gln---- | 38 |
| QY | 229 | CCCCACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAAGCTCTGTGACCTG | 288 |
| DB | 38 | ----- | 38 |
| QY | 289 | GAGCAGCAGCGCCATCTCTGGGCTTCTAGTCTTCTCCAGAGCACAAGGACTCTGGGTCT | 348 |
| DB | 38 | ----- | 38 |
| QY | 349 | GACCTCACTGTTCTGGNAGACATGGGGGCTTAGAGTCCTAAACAGACTGTTTCCCCCT | 408 |
| DB | 38 | ----- | 38 |
| QY | 409 | TCCAGCAGAGAAAGAGTCTGAAGAGCCACCAAGCTGCAGCCCGCAGCTCTAGCAG | 468 |
| DB | 39 | -----ArgLysGluSerLysLysProAlaAlaLysLeuLysProArgAlaLeuGluG | 56 |
| QY | 469 | GCTGGCTCCGCGGAGATGGAGTCAAGCAGAGGGCGCAGAGGATGAATCGGAAGTCC | 528 |
| DB | 56 | lyTrpLeuGlyProGluAspSerGlyGluValGluGlyThrGluAspLysLeuGluIleA | 76 |
| QY | 529 | GG 530 | |
| DB | 76 | ==== | 76 |

| | | |
|------------|-----------------|-----------------------------------|
| RESULT 13 | | |
| GHRL BOVIN | | |
| ID | GHRL BOVIN | STANDARD; |
| AC | Q9BDJ6; Q9GKY6; | PRT; 116 AA. |
| DT | 28-FEB-2003 | (Rel. 41, Created) |
| DT | 28-FEB-2003 | (Rel. 41, Last sequence update) |
| DT | 05-JUL-2004 | (Rel. 44, Last annotation update) |

Ghrelin precursor (growth hormone secretagogue) (Growth hormone releasing peptide).
Name=GHRL;
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
Kita K., Harada K., Yokota H.;
Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE OF 24-99 FROM N.A.
Kojima M.;
RA
Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specific ligand for the growth hormone secretagogue receptor type 1 (GHSR) inducing the release of growth hormone from the pituitary. Has an appetite-stimulating effect, induces adiposity and stimulates gastric acid secretion. Involved in growth regulation (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- PMW: O-n-octanoylation is essential for activity (By similarity).

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CC
CC -!- SIMILARITY: Belongs to the motillin family.
CC

CC or send an email to license@isp-slp.ch .

CC

| | | | |
|----|-------------------------------------------------------------------|---------|-----------------------------------|
| DR | EMBL; AB060699; BAC75928.1; -. | | |
| DR | GO; GO:0005576; C:extracellular; IEA. | | |
| DR | GO; GO:0016608; F:growth hormone-releasing hormone activity; IEA. | | |
| DR | GO; GO:0050791; P:regulation of physiological process; IEA. | | |
| DR | InterPro; IPR006737; motilin assoc. | | |
| DR | InterPro; IPR006738; motilin ghrelin. | | |
| DR | InterPro; IPR005441; Preproghrelin. | | |
| DR | Pfam; PF04643; Motilin assoc; 1. | | |
| DR | Pfam; PF04644; Motilin ghrelin; 1. | | |
| DR | PRINTS; PR01624; GHRELIN. | | |
| DR | ProDom; PD332162; Preproghrelin; 1. | | |
| DR | Signal. | | |
| FT | SIGNAL. | 1 | 23 Potential. |
| FT | CHAIN | 24 | 50 ghrelin. |
| SQ | SEQUENCE | 116 AA; | 12977 MW; E78ECA3DBF0E568E CRC64; |

| | |
|------------------------|----------|
| Alignment Scores: | |
| Pred. No.: | 1.52e-08 |
| Score: | 206.50 |
| Percent Similarity: | 43.26% |
| Best Local Similarity: | 36.17% |
| Query Match: | 20.05% |
| DB: | 2 |
| Gaps: | 1 |
| Indels: | 67 |
| Mismatches: | 13 |
| Conservative: | 10 |
| Matches: | 51 |
| Length: | 116 |

US-10-659-782A-11 (1-579) x Q863L0 (1-116)

Qy 112 ATGCGCTCCCAAGGACCGTCTCGAGCCTCTGTCTCTCGCATGCCTCTGGTGACTGG 171
|||||:|||||||:|||||:|||||:|||||:|||||:
Db 1 MetProAlaProArThrIleTySerLeuLeuLeuSerLeuLeuTrpMetAspLeu 20

| Qy | 172 | GCCATGCGAGGCTCCAGCTTCTGAGCGCCTGAACACACAGAGAGATCCAGGTGAGACCTCCC | 231 |
|----|-----|----------------------------------------------------------------|-----|
| Db | 21 | AlaMetAlaGlySerSerPheLeuSerProGluHisGlnIvsLeuGln | 36 |

232 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCAAGCTCTGTGTGACCTGGAG 291

D_b 36

QY 292 CAGCAGCGGCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 351

Db 36

QY 352 CTCAC TGTTTCTGGAAGGACATGGGGGCTTAGAGTCTTAAACAGACTGTTTCCCCCTTCC 411

db 36 ----- 36

[illegible]

| | | |
|----|-----|-----------------------------------------------------------------------|
| DB | 37 | ---Arg--LysGluProLysLysProSerGlyArgLeuLysProArgAlaLeuGluGlyG 55 |
| QV | 472 | GGCTCGGCCCCGCGACGATGCGCGCTCAGCAGACCCCCCGACGCGTCTCAACTCTCAACTCTCCG 530 |

| | | | |
|----|-----|-----------------------------------------------------------------|-----|
| QY | 4/2 | GGCTCCGCCCGGAAAGATGGAGGTCAAGCAGAGAGGGGGCAGAGGGATGAATCGGAAGTCCGG | 530 |
| D6 | 55 | LnphAsnProAspVa[G]vSerdnGnGnGnGnGnVAlaGnAsnGnLnGnGnLnLeArg | 74 |

DD 33 INFNEASPFLOASPFVAGRYCEGFGINGCNGNGRYAGAGUASPGUNBENGUNREAR 74

RESULT 15

Q6TGF0 PRELIMINARY; PRT; 65 AA.
ID Q6TGF0

AC Q6TGF0;
DT 05-JUL-2004 (TREMBLREL. 27, Created)

| DT | 05-JUL-2004 (TREMBlrel. 27, Last sequence update) |
|----|-----------------------------------------------------|
| DT | 05-JUL-2004 (TREMBlrel. 27, Last annotation update) |

DE Ghrelin (Fragment).
OS Sus scrofa (Pig).
OS

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCNT NCNT 2022

```

OX NCBI_TaxID=9823;
RN [1]
PD SEQUENCE FROM N A

```

LIU D., ZHANG Y., ZHANG X., YANG G.;
 Submitted (SEP-2003) to the EMBL/GenBank/DBI databases

DR EMBL; AY422043; AAQ97622.1; -;
DR InterPro: IPR006738; motif in chrelin.
DR submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.

DR InterPro; IPR005441; Preproghrelin.

DR pfam: PF04644; Motilin ghrelin; 1.
DR PRINTS; PR01624; GHRELIN.
FT NON_TER 1 1
FT NON_TER 65 65
SQ SEQUENCE 65 AA; 6979 MW; 55D3713C501444D5 CRC64;

Alignment Scores:

| | | | |
|------------------------|---------|---------------|----|
| Pred. No.: | 1.4e-06 | Length: | 65 |
| Score: | 182.50 | Matches: | 48 |
| Percent Similarity: | 42.64% | Conservative: | 7 |
| Best Local Similarity: | 37.21% | Mismatches: | 7 |
| Query Match: | 17.72% | Indels: | 67 |
| DB: | 2 | Gaps: | 2 |

US-10-659-782A-11 (1-579) x Q6TGF0 (1-65)

| | | | |
|----|-----|-------------------------------------------------------------|-----|
| QY | 124 | GGGACCGCTGCGAGCCTCTGCTCTCGGCATGCTCTGGCTG---GACTTGGCCATGGCA | 180 |
| Db | 2 | GlyThrIleCysSerLeuLeuLeuSerValLeuMetAlaaspLeuAlaMetAla | 21 |
| QY | 181 | GGCTCCAGCTTCTGAGCCCTGAACACACAGAGTCCAGGTGAGACCTCCCCACAAAGCC | 240 |
| Db | 22 | GlySerSerPheLeuSerProGluHisGlnLysValGln--Gln----- | 35 |
| QY | 241 | CCACATGTTGTTCCAGCCCTGCCACTTAGCAACCACTCTGTGACCTGGAGCAGCAGCGC | 300 |
| Db | 35 | ----- | 35 |
| QY | 301 | CATCTCTGGGCTTACGTCTTCTCCAGAGACAAAGGACTCTGGGTCTGACCTCACTGTT | 360 |
| Db | 35 | ----- | 35 |
| QY | 361 | TCTGGAAGGACATGGGGGCTTAGAGTCTTAAACAGACTGTTTCCCTTCCAGCAGAGAA | 420 |
| Db | 36 | -----ArgL | 37 |
| QY | 421 | AGGAGTCGAAGAGCCACCAAGCTGCAGCCCGAGCTCTAGCAGGCTGGCTCCGCC | 480 |
| Db | 37 | YsGluSerLysLysProAlaLysLeuLysProArgAlaLeuGluGlyTrpLeuGlyP | 57 |
| QY | 481 | CGGAAGATGGAGGTCAAGCAGAA | 503 |
| Db | 57 | roGluaspSerGlyGluValGlu | 64 |

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Job time : 164.5 secs

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